Amendment to the Specification:

Please delete the previously filed Sequence Listing and insert the substitute Sequence Listing filed herewith.

Please replace paragraph [0049] with the following amended paragraph:

[0049] Such polypeptides can be produced in E. coli in good yield and have been shown to adopt random coil or β-sheet structures (Krejchi et al.. Science, 265:1427-1432 (1994) and McGrath et al., J. Am. Chem. Soc. 114:727-733 (1992). The periodic acidic side chains from the glutamic acid residues provide affinity to basic surfaces. The natural domain is a bacterial phosphotriesterase which catalyzes rapid hydrolysis of organophosphorus pesticides and nerve agents. The phosphotriesterase used here contains the modified amino acid sequence reported by Mulbry and coworkers, which is characterized by deletion of the 33 Amino-terminal amino acids of the native enzyme (from native sequence of *pseudomonas diminuta*) and replacement by the first 5 lac Z residues (Met-Ile-Thr-Asn-Ser-) (SEQ ID NO:3) followed by the enzyme residues (-Gly-Asp-Arg-(SEQ ID NO:9)), in order to achieve significant improvements in the enzymatic activity in E. coli (Mulbry and Karns, J. Bacteriol. 171:6740-6746 (1989)). The activity of the enzyme can be easily determined using the pesticide paraoxon as substrate. Paraoxon can be enzymatically degraded to release a brightly colored phenolic product with a maximal absorption at 400 nm (Omburo et al., J. Biol. Chem. 267:13278-13283). The enzyme shows good stability and unusually high enzymatic activity, exhibiting a rate near the diffusion limit with substrate paraoxon (Caldwell et al., Biochemistry, 30:7438-7444 (1991)). The fusion proteins containing the repetitive polypeptides and phosphotriesterase adsorb to basic surfaces through the acidic artificial domain while the partner enzyme catalyzes hydrolysis of organophosphates.